



## SEQUENCE LISTING

<110> MacPhee, Colin Houston  
Tew, David Graham  
Southan, Christopher Donald  
Hickey, Deirdre Mary Bernadette  
Gloge, Israel Simon  
Lawrence, Geoffrey Mark Prouse  
Rice, Simon Quentyn John

<120> Lipoprotein Associated Phospholipase A2,  
Inhibitors Thereof and Use of the Same in Diagnosis and  
Therapy

| <130> P30693C4X1C1

<140> 09/922,067  
<141> 2001-08-03

<150> 09/193,130  
<151> 2000-11-28

<150> 08/387,858  
<151> 1994-06-24

<150> PCT/GB94/01374  
<151> 1994-06-24

<150> GB 9313144.9  
<151> 1993-06-25

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 37  
<212> PRT  
<213> Homo sapien

<400> 1  
Met Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Ala Ala Ile Asp Leu  
1 5 10 15  
Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His  
20 25 30  
Lys Asp Phe Asp Gln  
35

<210> 2  
<211> 30  
<212> PRT  
<213> Homo sapien

<400> 2  
Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro  
1 5 10 15  
Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn

```

<210> 3
<211> 27
<212> PRT
<213> Homo sapien

<400> 3
Gln Tyr Ile Asn Pro Ala Val Met Ile Thr Ile Arg Gly Ser Val His
 1           5           10          15
Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly
 20           25

<210> 4
<211> 19
<212> PRT
<213> Homo sapien

<400> 4
Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr
 1           5           10          15
Pro Ala Asn

<210> 5
<211> 420
<212> DNA
<213> Unknown

<220>
<221> misc_feature
<222> 265, 390, 395, 403, 406
<223> n = A,T,C or G

<400> 5
aaaaaaaaaccta ttttaatcctt aattgttattt ctctattccctt gaagagttctt gtaacatgtat 60
gtgttgatttgg ttgtgtttaa ttgttgtccc ttggataaga ttctcatcat ctccttcaat 120
caaggcgtcc cactgatcaa aatctttatg aagtccctaaa tgctttgtt agaatgctaa 180
tgaagcttttgg ttgctaaatgat caatacgctgc atttgaatctt atgtctccctt ttaatttgag 240
catgtgtcca attattttgc cagtnngcaaa agtgaagtcg gcaaaattctt ggtggactgaa 300
acccttgattt gtaatcatctt ttctttctttt atcaggtttagt tagcattttt tcatttttat 360
gatatttagca ggatatttggaa aatattcagn gttgntaaaa agnngnggctt gagggattctt 420

<210> 6
<211> 379
<212> DNA
<213> Unknown

<220>
<221> misc_feature
<222> 84
<223> n = A,T,C or G

<400> 6
tgcttaatatc ataaaaatgta aaaaatgcta ctcacctgat aaagaaaagaa agatgattac 60

```

aatcaggggt tcagtccacc agantttgc tgacttcaact tttgcaactg gcaaaataat 120  
 tggacacatg ctcaaattaa agggagacat agattcaa at gtagctattg atcttagcaa 180  
 caaagcttca ttagcattct tacaaaagca tttaggactt cataaaagatt ttgttcagtg 240  
 ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300  
 caattcaaca catcatgtt acagaacttc ttccagggaa taggaggaaa tacaattggg 360  
 gtttaaaaata ggaaaaata 379

<210> 7  
 <211> 279  
 <212> DNA  
 <213> Unknown

<220>  
 <221> misc\_feature  
 <222> 257  
 <223> n = A,T,C or G

<400> 7  
 gaagaatgca tttagattaa agtttgatat ggaacaactg aaggactcta ttgataggg 60  
 aaaaatagca gtaattggac attctttgg tggagcaacg gttattcaga ctcttagtga 120  
 agatcagaga ttcagatgtg gtattgcctt ggatgcattt atgtttccac tgggtgatga 180  
 agtatattcc agaattcctc agccctctt ttttatcaac tctgaatatt tccaatatcc 240  
 tgctaatatc ataaaantgg aaaaatgcta ctcacctgg 279

<210> 8  
 <211> 572  
 <212> DNA  
 <213> Homo sapien

<400> 8  
 aaaatagcag taattggaca ttcttaggt ggagcaacgg ttattcagac tcttagtga 60  
 gatcagagat tcagatgtgg tattgcctg gatgcattt gttttccact gggtagtga 120  
 gtatattcca gaattcctca gcccctctt tttatcaact ctgaatattt ccaatatcc 180  
 gctaataatca taaaatgaa aaaatgctac tcacctgata aagaaagaaa gatgattaca 240  
 atcaggggtt cagtccacca gaatttgct gacttcactt ttgcaactgg caaaataatt 300  
 ggacacatgc tcaaattaaa gggagacata gattcaa atg tagtatttga tcttagcaac 360  
 aaagcttcat cagcattctt aaaaaagcat ttaggactt ataaagattt tgatcattgg 420  
 gactgcttga ttgaaggaga tgatgagaat cttattccag ggaccaacat taacacaacc 480  
 aatcaacaca tcatgttaca gaactcttca ggaatagaga aatacaatta ggattaaaat 540  
 agttttta aaaaaaaaaa aaaaaaaaaact cg 572

<210> 9  
 <211> 1361  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> CDS  
 <222> (38) ... (1360)

<400> 9  
 tgagagacta agctgaaact gctgctcagc tcccaag atg gtg cca ccc aaa ttg 55  
 Met Val Pro Pro Lys Leu  
 1 5

cat gtg ctt ttc tgc ctc tgc ggc tgc ctg gct gtg gtt tat cct ttt 103  
 His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe  
 10 15 20

gac tgg caa tac ata aat cct gtt gcc cat atg aaa tca tca gca tgg			151
Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp			
25	30	35	
gtc aac aaa ata caa gta ctg atg gct gct gca agc ttt ggc caa act			199
Val Asn Lys Ile Gln Val Leu Met Ala Ala Ser Phe Gly Gln Thr			
40	45	50	
aaa atc ccc cgg gga aat ggg cct tat tcc gtt ggt tgc aca gac tta			247
Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu			
55	60	65	70
atg ttt gat cac act aat aag ggc acc ttc ttg cgt tta tat tat cca			295
Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro			
75	80	85	
tcc caa gat aat gat cgc ctt gac acc ctt tgg atc cca aat aaa gaa			343
Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu			
90	95	100	
tat ttt tgg ggt ctt agc aaa ttt ctt gga aca cac tgg ctt atg ggc			391
Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly Thr His Trp Leu Met Gly			
105	110	115	
aac att ttg agg tta ctc ttt ggt tca atg aca act cct gca aac tgg			439
Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr Pro Ala Asn Trp			
120	125	130	
aat tcc cct ctg agg cct ggt gaa aaa tat cca ctt gtt gtt ttt tct			487
Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser			
135	140	145	150
cat ggt ctt ggg gca ttc agg aca ctt tat tct gct att ggc att gac			535
His Gly Leu Gly Ala Phe Arg Thr Leu Tyr Ser Ala Ile Gly Ile Asp			
155	160	165	
ctg gca tct cat ggg ttt ata gtt gct gct gta gaa cac aga gat aga			583
Leu Ala Ser His Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg			
170	175	180	
tct gca tct gca act tac tat ttc aag gac caa tct gct gca gaa ata			631
Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp Gln Ser Ala Ala Glu Ile			
185	190	195	
ggg gac aag tct tgg ctc tac ctt aga acc ctg aaa caa gag gag gag			679.
Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr Leu Lys Gln Glu Glu Glu			
200	205	210	
aca cat ata cga aat gag cag gta cgg caa aga gca aaa gaa tgt tcc			727
Thr His Ile Arg Asn Glu Gln Val Arg Gln Arg Ala Lys Glu Cys Ser			
215	220	225	230
caa gct ctc agt ctg att ctt gac att gat cat gga aag cca gtg aag			775
Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp His Gly Lys Pro Val Lys			
235	240	245	
aat gca tta gat tta aag ttt gat atg gaa caa ctg aag gac tct att			823
Asn Ala Leu Asp Leu Lys Phe Asp Met Glu Gln Leu Lys Asp Ser Ile			
250	255	260	

gat agg gaa aaa ata gca gta att gga cat tct ttt ggt gga gca acg		871	
Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr			
265	270	275	
gtt att cag act ctt agt gaa gat cag aga ttc aga tgt ggt att gcc		919	
Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala			
280	285	290	
ctg gat gca tgg atg ttt cca ctg ggt gat gaa gta tat tcc aga att		967	
Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile			
295	300	305	310
cct cag ccc ctc ttt ttt atc aac tct gaa tat ttc caa tat cct gct		1015	
Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala			
315	320	325	
aat atc ata aaa atg aaa tgc tac tca cct gat aaa gaa aga aag		1063	
Asn Ile Ile Lys Met Lys Cys Tyr Ser Pro Asp Lys Glu Arg Lys			
330	335	340	
atg att aca atc agg ggt tca gtc cac cag aat ttt gct gac ttc act		1111	
Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr			
345	350	355	
ttt gca act ggc aaa ata att gga cac atg ctc aaa tta aag gga gac		1159	
Phe Ala Thr Gly Lys Ile Ile Gly His Met Leu Lys Leu Lys Gly Asp			
360	365	370	
ata gat tca aat gca gct att gat ctt agc aac aaa gct tca tta gca		1207	
Ile Asp Ser Asn Ala Ala Ile Asp Leu Ser Asn Lys Ala Ser Leu Ala			
375	380	385	390
tcc tta caa aag cat tta gga ctt cat aaa gat ttt gat cag tgg gac		1255	
Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln Trp Asp			
395	400	405	
tgc ttg att gaa gga gat gat gag aat ctt att cca ggg acc aac att		1303	
Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu Ile Pro Gly Thr Asn Ile			
410	415	420	
aac aca acc aat caa cac atc atg tta cag aac tct tca gga ata gag		1351	
Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly Ile Glu			
425	430	435	
aaa tac aat t		1361	
Lys Tyr Asn			
440			

<210> 10  
<211> 7  
<212> PRT  
<213> Homo sapien

<400> 10  
Gln Tyr Ile Asn Pro Val Ala  
1 5

<210> 11  
<211> 20  
<212> PRT  
<213> Homo sapien

<400> 11  
Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr  
1 5 10 15  
Phe Ala Thr Gly  
20

<210> 12  
<211> 7  
<212> PRT  
<213> Homo sapien

<400> 10  
Gln Tyr Ile Asn Pro Ala Val  
1 5

<210> 13  
<211> 5  
<212> PRT  
<213> Homo sapien

<400> 10  
Gln Tyr Ile Asn Pro  
1 5